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#2

10/09

OIPE

## RAW SEQUENCE LISTING

DATE: 06/07/2001

PATENT APPLICATION: US/09/854,356

TIME: 17:01:19

Input Set : C:\PAOLA\09854356.txt

Output Set: C:\CRF3\06072001\I854356.raw

ENTERED

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3 <110> APPLICANT: Cheever, Martin A.
4      Gheysen, Dirk
5      Corixa Corporation
6      SmithKline Beecham Biologicals S. A.
8 <120> TITLE OF INVENTION: HER-2/neu Fusion Proteins
10 <130> FILE REFERENCE: 014058-009810PC
12 <140> CURRENT APPLICATION NUMBER: 09/854,356
13 <141> CURRENT FILING DATE: 2001-05-09
15 <150> PRIOR APPLICATION NUMBER: US 09/493,480
16 <151> PRIOR FILING DATE: 2000-01-28
18 <150> PRIOR APPLICATION NUMBER: US 60/117,976
19 <151> PRIOR FILING DATE: 1999-01-29
21 <160> NUMBER OF SEQ ID NOS: 26
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1255
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <223> OTHER INFORMATION: human HER-2/neu protein
33 <220> FEATURE:
34 <221> NAME/KEY: DOMAIN
35 <222> LOCATION: (1)..(653)
36 <223> OTHER INFORMATION: extracellular domain (ECD)
38 <220> FEATURE:
39 <221> NAME/KEY: DOMAIN
40 <222> LOCATION: (676)..(1255)
41 <223> OTHER INFORMATION: intracellular domain (ICD)
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44 <221> NAME/KEY: DOMAIN
45 <222> LOCATION: (990)..(1255)
46 <223> OTHER INFORMATION: phosphorylation domain (PD)
48 <220> FEATURE:
49 <221> NAME/KEY: DOMAIN
50 <222> LOCATION: (990)..(1048)
51 <223> OTHER INFORMATION: fragment of the phosphorylation domain, preferred
52    portion (delta PD)
54 <400> SEQUENCE: 1
55 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
56   1             5             10             15
58 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
59             20             25             30
61 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
62             35             40             45
64 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
65             50             55             60
67 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val

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68 65          70          75          80
70 Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
71          85          90          95
73 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
74          100          105          110
76 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
77          115          120          125
79 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
80          130          135          140
82 Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
83 145          150          155          160
85 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
86          165          170          175
88 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
89          180          185          190
91 His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
92          195          200          205
94 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
95          210          215          220
97 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
98 225          230          235          240
100 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
101          245          250          255
103 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
104          260          265          270
106 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
107          275          280          285
109 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
110          290          295          300
112 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
113 305          310          315          320
115 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
116          325          330          335
118 Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
119          340          345          350
121 Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
122          355          360          365
124 Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
125          370          375          380
127 Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
128 385          390          395          400
130 Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
131          405          410          415
133 Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
134          420          425          430
136 Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
137          435          440          445
139 Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
140          450          455          460

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```

142 Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
143 465 470 475 480
145 Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
146 485 490 495
148 Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
149 500 505 510
151 Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
152 515 520 525
154 Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
155 530 535 540
157 Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
158 545 550 555 560
160 Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
161 565 570 575
163 Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
164 580 585 590
166 Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
167 595 600 605
169 Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
170 610 615 620
172 Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
173 625 630 635 640
175 Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser
176 645 650 655
178 Ala Val Val Gly Ile Leu Leu Val Val Leu Gly Val Val Phe Gly
179 660 665 670
181 Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
182 675 680 685
184 Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
185 690 695 700
187 Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
188 705 710 715 720
190 Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
191 725 730 735
193 Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
194 740 745 750
196 Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
197 755 760 765
199 Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
200 770 775 780
202 Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
203 785 790 795 800
205 Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg
206 805 810 815
208 Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
209 820 825 830
211 Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
212 835 840 845
214 Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe

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```

215      850      855      860
217 Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
218 865      870      875      880
220 Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
221      885      890      895
223 Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
224      900      905      910
226 Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
227      915      920      925
229 Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
230      930      935      940
232 Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
233 945      950      955      960
235 Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
236      965      970      975
238 Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
239      980      985      990
241 Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
242      995      1000      1005
244 Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu
245      1010      1015      1020
247 Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly
248 1025      1030      1035      1040
250 Gly Met Val His His Arg His Arg Ser Ser Thr Arg Ser Gly Gly
251      1045      1050      1055
253 Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg
254      1060      1065      1070
256 Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly
257      1075      1080      1085
259 Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His
260      1090      1095      1100
262 Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu
263 1105      1110      1115      1120
265 Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln
266      1125      1130      1135
268 Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
269      1140      1145      1150
271 Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
272      1155      1160      1165
274 Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
275      1170      1175      1180
277 Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
278 1185      1190      1195      1200
280 Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala
281      1205      1210      1215
283 Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
284      1220      1225      1230
286 Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
287      1235      1240      1245

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Input Set : C:\PAOLA\09854356.txt

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289 Leu Gly Leu Asp Val Pro Val
290     1250                      1255
293 <210> SEQ ID NO: 2
294 <211> LENGTH: 1256
295 <212> TYPE: PRT
296 <213> ORGANISM: Rattus sp.
298 <220> FEATURE:
299 <223> OTHER INFORMATION: rat HER-2/neu protein
301 <220> FEATURE:
302 <221> NAME/KEY: DOMAIN
303 <222> LOCATION: (1)..(654)
304 <223> OTHER INFORMATION: extracellular domain (ECD)
306 <220> FEATURE:
307 <221> NAME/KEY: DOMAIN
308 <222> LOCATION: (677)..(1256)
309 <223> OTHER INFORMATION: intracellular domain (ICD)
311 <220> FEATURE:
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313 <222> LOCATION: (721)..(998)
314 <223> OTHER INFORMATION: kinase domain (KD)
316 <220> FEATURE:
317 <221> NAME/KEY: DOMAIN
318 <222> LOCATION: (991)..(1256)
319 <223> OTHER INFORMATION: phosphorylation domain (PD)
321 <220> FEATURE:
322 <221> NAME/KEY: DOMAIN
323 <222> LOCATION: (991)..(1049)
324 <223> OTHER INFORMATION: fragment of the phosphorylation domain, preferred
325     portion (delta PD)
327 <400> SEQUENCE: 2
328 Met Glu Leu Ala Ala Trp Cys Arg Trp Gly Phe Leu Leu Ala Leu Leu
329     1                      5                      10                      15
331 Pro Pro Gly Ile Ala Gly Thr Gln Val Cys Thr Gly Thr Asp Met Lys
332     20                      25                      30
334 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
335     35                      40                      45
337 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
338     50                      55                      60
340 Val Pro Ala Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
341     65                      70                      75                      80
343 Gln Gly Tyr Met Leu Ile Ala His Asn Gln Val Lys Arg Val Pro Leu
344     85                      90                      95
346 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Lys Tyr
347     100                     105                     110
349 Ala Leu Ala Val Leu Asp Asn Arg Asp Pro Gln Asp Asn Val Ala Ala
350     115                     120                     125
352 Ser Thr Pro Gly Arg Thr Pro Glu Gly Leu Arg Glu Leu Gln Leu Arg
353     130                     135                     140
355 Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Arg Gly Asn Pro

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VERIFICATION SUMMARY

DATE: 06/07/2001

PATENT APPLICATION: US/09/854,356

TIME: 17:01:21

Input Set : C:\PAOLA\09854356.txt

Output Set: C:\CRF3\06072001\I854356.raw